



A-378CIP5C (3-31-04).ST25
SEQUENCE LISTING



<110> BOYLE, WILLIAM J.
LACEY, DAVID LEE
CALZONE, FRANK J.
CHANG, MING-SHI
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

<130> A-378CIP5C

<140> US 09/613,591

<141> 2000-07-10

<150> US 09/457,647

<151> 1999-12-09

<150> US 09/350,670

<151> 1999-07-09

<150> US 08/706,945

<151> 1996-09-03

<150> US 08/577,788

<151> 1995-12-22

<160> 178

<170> PatentIn version 3.2

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<211> 36

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gactagtccc acaatgaaca agtggctgtg 30

<210> 10
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<220>
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<400> 11
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<210> 12
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<220>
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<400> 12
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<210> 13
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<400> 13
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<210> 14
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<400> 14
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<210> 15
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<400> 15
 caagacacct tgaagggcct gatg 24

<210> 16
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 <400> 17
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 <210> 23
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<210> 24
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 <210> 25
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 <400> 26
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 <210> 27
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 <210> 30
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A-378CIP5C (3-31-04).ST25

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<210> 31
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 <213> Mus musculus

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Gln Leu Leu

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<400> 33
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<210> 34
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<400> 36
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<210> 37
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 <213> Homo sapiens

A-378CIP5C (3-31-04).ST25

<400> 37		
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cctctgcggc cgccagggtg acatctattc cac		33
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A-378CIP5C (3-31-04).ST25

<211> 35
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 gcgagaggac tcctcctgtt taggcggccc tcgcctaaac ttgcaacgct tcgttgccgg 180
 gcctcccacc gcccgtcctg cgggcgggtat ttgacggtcc gtagtttaaat tcgtcttccg 240
 gtaggactgc ctaccggaaa aacgcaaaga tgtttgagaa aacaaataaa aagattttatg 300
 taagtttata cctgcagcat gaattgaaaa tttcataccc gttagttaac gaggacaatt 360
 ttaacgaaat ctttatgaaa ccgtcgccaa acaacataac tcaaagtaaa cgcgtaacca 420
 atttaccttt cactggcacg cgaatgatgt cggattataa aaactttata gggttctcga 480
 aaaaggaagc gtacgggtgc gatttgtaag aaaaagagaa aaccaattta gcaacaaact 540
 aaataataaa cgatataaat aaaaagctat taatagttga tctcttcctt gttaattacc 600
 atacaagtat gtgcgtacat ttttatttga tagatatatc aacagaaaga gacttacacg 660
 ttttgattcg taaggcttcg gtaataatcg tcatacttat ccctttgatt tgggtcacta 720
 ttctggacta ctaaagcgaa gaaattaatg taaacctcta aaaaataaat gtcgtaacaa 780
 aagtttatat aagggttaatt agccacttac taacctcaat cttattagat gatatcctag 840
 tataaaataa tttaatcgca gtagtattat aacggaggta aaaaatccca ttaataggtc 900
 ttaactttat agtctaaatt ggtatcttac tcctatttac tagcgctcat ttattataag 960
 tgttacatgg taaaatcagt atagtctatt cgtaactaat tataagtaata acgaagatgt 1020
 ccgaaattaa aataattaat aagacattca cagcagccgt aaatacagaa agtatgggta 1080
 gagaaatagg aatggataac aaacagcggt caaaacgcac aatatatagt aattttgcca 1140
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 tatgttaaca aattgtattc atggacatcc tagcatgtcc aaatgcgttc ttttaccaaa 1260
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 gtataccaat tgcgcaacct taagctcgag tgatcacagc tggacgtccc atggtacctt 1380
 cgaatgagct cctaggcgcc tttcttcttc ttcttcttct ttcgggcttt ctttcgactc 1440
 aaccgacgac ggtggcgact cgttattgat cgtattgggg aaccccgag atttgcccag 1500
 aactcccaa aaaacgactt tcctccttgg cgagaagtgc gagaagtg 1548

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<210> 48
 <211> 55
 <212> DNA
 <213> Artificial Sequence
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 <223> pAMG21
 <400> 48
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<210> 49
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 <212> DNA
 <213> Artificial Sequence
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 <223> pAMG21
 <400> 49
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<210> 50
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 ctcttgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccggg 180
 ggggtggcggg caggacgccc gccataaact gccaggcatc aaattaagca gaaggccatc 240
 ctgacggatg gccttttttg gtttctacaa actcttttgt ttatttttct aaatacatc 300
 aaatatggac gtcgtactta acttttaaa gttgggcaat caattgctcc tgttaaaatt 360
 gcttttagaaa tactttggca gcggtttggt gtattgagtt tcatttgcgc attggttaaa 420
 tggaaagtga ccgtgcgctt actacagcct aatatttttg aaatatccca agagcttttt 480
 ccttcgcatg cccacgctaa acattctttt tctcttttgg ttaaatcggt gtttgattta 540

A-378CIP5C (3-31-04).ST25

ttatttgcta tatttatttt tcgataatta tcaactagag aaggaacaat taatggtatg	600
ttcatacag catgtaaaaa taaactatct atatatgtgt ctttctctga atgtgcaaaa	660
ctaagcattc cgaagccatt attagcagta tgaataggga aactaaacc agtgataaga	720
cctgatgatt tcgcttcttt aattacattt ggagattttt tatttacagc attgttttca	780
aatatattcc aattaatcgg tgaatgattg gagttagaat aatctactat aggatcatat	840
tttattaaat tagcgtcatc ataattattgc ctccattttt tagggtaatt atccagaatt	900
gaaatatcag atttaacatc agaatgagga taaatgatcg cgagtaaata atattcacia	960
tgtaccattt tagtcatatc agataagcat tgattaatat cattattgct tctacaggct	1020
ttaattttat taattattct gtaagtgtcg tcggcattta tgtctttcat acccatctct	1080
ttatccttac ctattgtttg tcgcaagttt tgcgtgttat atatcattaa aacggtaata	1140
gattgacatt tgattctaataaattggatt tttgtcacac tattatatcg cttgaaatac	1200
aattgtttta cataagtacc tgtaggatcg tacagggtta cgcaagaaaa tggtttggtta	1260
tagtcgatta atcgatttga ttctagattt gttttaacta attaaaggag gaataacata	1320
tggttaacgc gttggaattc gagctcacta gtgtcgacct gcagggtacc atggaagctt	1380
actcgaggat ccgcggaaag aagaagaaga agaagaaagc ccgaaaggaa gctgagttgg	1440
ctgctgccac cgctgagcaa taactagcat aacccttggttggcctctaaa cgggtcttga	1500
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAMG22

<400> 51	
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<210> 52
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAMG22

<400> 52	
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<210> 53
 <211> 141
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAMG22

<400> 53

A-378CIP5C (3-31-04).ST25

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acatacagat aaccatctgc ggtgataaat tatctctggc ggtgttgaca taaataccac	120
tggcggtgat actgagcaca t	141

<210> 54
 <211> 147
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAMG22

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tttttgatg tctattggt gacgccacta tttaatagag accgccacaa ctgtatttat	120
ggtgaccgcc actatgactc gtgtagc	147

<210> 55
 <211> 55
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAMG22

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<210> 56
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAMG22

<400> 56	
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<210> 57
 <211> 668
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<220>
 <223> pAMG22

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gcgagaggac tcatcctgtt taggcggccc tcgcctaaac ttgcaacgct tcgttgccgg	180
gcctcccacc gcccgctctg cgggcgggtat ttgacggtcc gtagtttaaat tcgtcttccg	240
gtaggactgc ctaccgaaa aacgcaaaga tgtttgagaa aacaaataaa aagatttatg	300
taagtttata cctgcagagt attaaaaatt ttttaagtaa actgtttacg attttaagaa	360

A-378CIP5C (3-31-04).ST25

ctaattataa gagttaacac tcgcgagtgt taaatagcta aactaagatc taaactcaat	420
tgattaatTTT cctccttatt gtataccaat tgcgcaacct taagctcgag tgatcacagc	480
tggacgtccc atgggtacct cgaatgagct cctagggcgcc tttcttcttc ttcttcttct	540
ttcggggcttt ccttcgactc aaccgacgac ggtggcgact cgttattgat cgtattgggg	600
aaccccggag atttgcccag aactcccca aaaacgactt tcctccttgg cgagaagtgc	660
gagaagtg	668

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 <212> DNA
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<220>
 <223> pAMG22

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ctcctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccgga	180
gggtggcggg caggacgcc gccataaact gccaggcatc aaattaagca gaaggggcct	240
cccaccgccc gtcctgcggg cgggtatttga cgggtccgtag tttaattcgt cttcgccatc	300
ctgacggatg gcctttttgc gtttctacaa actcttttgt ttatttttct aaatacatc	360
aaatatggac gtctcataat ttttaaaaaa ttcatttgac aaatgctaaa attcttgatt	420
aatatttctca attgtgagcg ctcacaattt atcgatttga ttctagattt gttttaacta	480
attaaaggag gaataacata tgggttaacgc gttggaattc gagctcacta gtgtcgacct	540
gcaggggtacc atggaagctt actcgaggat ccgcggaaag aagaagaaga agaagaaagc	600
ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa taactagcat aacccttgg	660
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tcacgc	726

<210> 59
 <211> 44
 <212> DNA
 <213> Homo sapiens

<400> 59	
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<210> 60
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 60	
gtcctcctgg tacctaccta aaacaac	27

<210> 61

A-378CIP5C (3-31-04).ST25

<211> 54
<212> DNA
<213> Homo sapiens

<400> 61
tatggatgaa gaaacttctc atcagctgct gtgtgataaa tgtccgccgg gtac 54

<210> 62
<211> 19
<212> PRT
<213> Homo sapiens

<400> 62
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1 5 10 15

Gly Thr Tyr

<210> 63
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

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gtgtgataaa tgtccgccgg gtac 84

<210> 64
<211> 78
<212> DNA
<213> Artificial Sequence

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ttggaggaaa agtttcca 78

<210> 65
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<220>
<223> pAMG21-MuOPG

<400> 65
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<210> 66
<211> 38
<212> DNA
<213> Artificial Sequence

A-378CIP5C (3-31-04).ST25

<220>
 <223> pAMG21-MuOPG

<400> 66
 gtgctcctgg tacctaccta aaacagcact gcacagtg 38

<210> 67
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 gtgtgataaa tgtgctccgg gtac 84

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<400> 69
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<210> 70
 <211> 48
 <212> DNA
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<400> 70
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 <212> DNA
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<220>
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<400> 71
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 gctgtgtgat aaatgtgctc cgggtac 87

<210> 72

A-378CIP5C (3-31-04).ST25

<211> 81
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 <220>
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 <212> DNA
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 <400> 74
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 <210> 75
 <211> 76
 <212> DNA
 <213> Mus musculus

 <400> 75
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 tgaacctgat tcccta 76

 <210> 76
 <211> 47
 <212> DNA
 <213> Mus musculus

 <400> 76
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 <210> 77
 <211> 43
 <212> DNA
 <213> Homo sapiens

 <400> 77
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<210> 79
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<400> 79
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<210> 80
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 <212> DNA
 <213> Mus musculus

<400> 80
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<220>
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<220>
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<210> 90	
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A-378CIP5C (3-31-04).ST25

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<220>
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<220>
<223> pAMG21-huOPG

<400> 93
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<210> 94
<211> 50
<212> DNA
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<223> pAMG21-huOPG

<400> 94
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<211> 50
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<220>
<223> pAMG21-huOPG

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A-378CIP5C (3-31-04).ST25

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<223> pAMG21-huOPG

<400> 97
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<210> 98
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A-378CIP5C (3-31-04).ST25

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<210> 104
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<210> 105
<211> 54
<212> DNA
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<400> 105
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<210> 106
<211> 31
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<400> 106
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<210> 107
<211> 44
<212> DNA
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<220>
<223> PCR primer for Fc-hOPG fusion protein.

<400> 107
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<210> 108
<211> 44
<212> DNA
<213> Artificial Sequence

<220>

A-378CIP5C (3-31-04).ST25

<223> PCR primer for FchOPG fusion protein.

<400> 108
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<210> 109
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc/muOPG

<400> 109
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<210> 110
<211> 39
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<220>
<223> Fc/muOPG

<400> 110
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<210> 111
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<400> 111
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<210> 112
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<220>
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<400> 112
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<210> 113
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<220>
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<400> 113
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A-378CIP5C (3-31-04).ST25

<212> DNA
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<220>
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<220>
 <223> pAMG21-huOPG

<220>
 <221> misc_feature
 <223> Linker with XbaI and KpnI sites inserted into human sequence.

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<210> 116
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 <212> DNA
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<220>
 <223> huOPG

<400> 116
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<210> 117
 <211> 62
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 117
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<210> 118
 <211> 62
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huOPG

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tt

62

<210> 119
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 119

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Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg
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Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
 35 40 45

Asp Trp His
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<210> 120
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 <213> Rattus rattus

<220>
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 <222> (124)..(1326)

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 aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc 168
 Met Asn Lys Trp Leu Cys Cys Ala Leu Val Phe Leu Asp Ile 15
 att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 216
 Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr 30
 gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 264
 Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly 45
 acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc 312
 Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val 60
 cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa 360
 Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu 75
 tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag 408
 Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln 85
 gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc 456
 Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg 105 110

A-378CIP5C (3-31-04).ST25

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Tyr	Leu	Glu	Leu	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	
			115					120					125			
ttg	ggt	gtg	ctg	cag	gct	ggg	acc	cca	gag	cga	aac	acg	ggt	tgc	aaa	552
Leu	Gly	Val	Leu	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	
		130					135					140				
aga	tgt	ccg	gat	ggg	ttc	ttc	tca	ggt	gag	acg	tca	tcg	aaa	gca	ccc	600
Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	
	145					150					155					
tgt	agg	aaa	cac	acc	aac	tgc	agc	tca	ctt	ggc	ctc	ctg	cta	att	cag	648
Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Ser	Leu	Gly	Leu	Leu	Leu	Ile	Gln	
160					165					170					175	
aaa	gga	aat	gca	aca	cat	gac	aat	gta	tgt	tcc	gga	aac	aga	gaa	gca	696
Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	
			180						185					190		
act	caa	aat	tgt	gaa	ata	gat	gtc	acc	ctg	tgc	gaa	gag	gca	ttc	ttc	744
Thr	Gln	Asn	Cys	Glu	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	
			195					200					205			
agg	ttt	gct	gtg	cct	acc	aag	att	ata	ccg	aat	tgg	ctg	agt	gtt	ctg	792
Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	
		210					215					220				
gtg	gac	agt	ttg	cct	ggg	acc	aaa	gtg	aat	gca	gag	agt	gta	gag	agg	840
Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	
	225					230					235					
ata	aaa	cgg	aga	cac	agc	tcg	caa	gag	caa	act	ttc	cag	cta	ctt	aag	888
Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	
240					245					250					255	
ctg	tgg	aag	cat	caa	aac	aga	gac	cag	gaa	atg	gtg	aag	aag	atc	atc	936
Leu	Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile	
				260					265					270		
caa	gac	att	gac	ctc	tgt	gaa	agc	agt	gtg	caa	cgg	cat	atc	ggc	cac	984
Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	Val	Gln	Arg	His	Ile	Gly	His	
			275					280					285			
gcg	aac	ctc	acc	aca	gag	cag	ctc	cgc	atc	ttg	atg	gag	agc	ttg	cct	1032
Ala	Asn	Leu	Thr	Thr	Glu	Gln	Leu	Arg	Ile	Leu	Met	Glu	Ser	Leu	Pro	
		290					295					300				
ggg	aag	aag	atc	agc	cca	gac	gag	att	gag	aga	acg	aga	aag	acc	tgc	1080
Gly	Lys	Lys	Ile	Ser	Pro	Asp	Glu	Ile	Glu	Arg	Thr	Arg	Lys	Thr	Cys	
	305					310					315					
aaa	ccc	agc	gag	cag	ctc	ctg	aag	cta	ctg	agc	ttg	tgg	agg	atc	aaa	1128
Lys	Pro	Ser	Glu	Gln	Leu	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	
320					325					330					335	
aat	gga	gac	caa	gac	acc	ttg	aag	ggc	ctg	atg	tac	gca	ctc	aag	cac	1176
Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	Tyr	Ala	Leu	Lys	His	
			340					345						350		
ttg	aaa	gca	tac	cac	ttt	ccc	aaa	acc	gtc	acc	cac	agt	ctg	agg	aag	1224
Leu	Lys	Ala	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	His	Ser	Leu	Arg	Lys	
			355					360					365			
acc	atc	agg	ttc	ttg	cac	agc	ttc	acc	atg	tac	cga	ttg	tat	cag	aaa	1272
Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Arg	Leu	Tyr	Gln	Lys	
		370					375					380				

A-378CIP5C (3-31-04).ST25

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Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser
    385                      390                      395

tgc tta tagttaggaa tggtcactgg gctgtttcctt caggatgggc caacactgat      1376
Cys Leu
    400

ggagcagatg gctgcttctc cggctcttga aatggcagtt gattcctttc tcatcagttg      1436
gtgggaatga agatcctcca gcccaacaca cacactgggg agtctgagtc aggagagtga      1496
ggcaggctat ttgataattg tgcaaagctg ccagggtgtac acctagaaag tcaagcaccc      1556
tgagaaagag gatattttta taacctcaaa cataggccct ttccttcctc tccttatgga      1616
tgagtactca gaaggcttct actatcttct gtgtcatccc tagatgaagg cctcttttat      1676
ttattttttt attctttttt tcggagctgg ggaccgaacc cagggccttg cgcttgcgag      1736
gcaagtgtc taccactgag ctaaactctc aaccctgaa ggcctctttc tttctgcctc      1796
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cccaatagtt tatccagctg tcatgcctgg ttcagtgctt actgactatg cgccctctta      2216
ttactgcatg cagtaattca actggaaata gtaataataa taatagaaat aaaatctaga      2276
ctccattgga tctctctgaa tatgggaata tctaacttaa gaagctttga gatttcagtt      2336
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aagactatta cagtattgct atttatatcc atccag                                2432

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<210> 121
 <211> 401
 <212> PRT
 <213> Rattus rattus

<400> 121

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
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Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
 50 55 60

A-378CIP5C (3-31-04).ST25

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80
 Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
 85 90 95
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
 100 105 110
 Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
 115 120 125
 Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140
 Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160
 Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
 165 170 175
 Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
 180 185 190
 Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205
 Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
 210 215 220
 Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255
 Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
 260 265 270
 Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala
 275 280 285
 Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly
 290 295 300
 Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
 305 310 315 320
 Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335

A-378CIP5C (3-31-04).ST25

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
340 345 350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 122
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<213> Mus musculus

<220>
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<222> (11)..(11)
<223> At position 11, R is a purine.

<220>
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<222> (91)..(1293)

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Met Asn Lys Trp Leu Cys Cys Ala
1 5
ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt 162
Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu
10 15 20
ctt cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg 210
Leu Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu
25 30 35 40
tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg 258
Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val
45 50 55
agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac 306
Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp
60 65 70
agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag 354
Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys
75 80 85
gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg 402
Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val
90 95 100
tgt gag tgt gag gaa ggg cgt tac ctg gag atc gaa ttc tgc ttg aag 450

A-378CIP5C (3-31-04).ST25																
Cys 105	Glu	Cys	Glu	Glu	Gly 110	Arg	Tyr	Leu	Glu	Ile 115	Glu	Phe	Cys	Leu	Lys 120	
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gag Glu	cga Arg	aac Asn	aca Thr 140	gtt Val	tgc Cys	aaa Lys	aaa Lys	tgt Cys 145	cca Pro	gat Asp	ggg Gly	ttc Phe	ttc Phe 150	tca Ser	ggt Gly	546
gag Glu	act Thr	tca Ser 155	tcg Ser	aaa Lys	gca Ala	ccc Pro	tgt Cys 160	ata Ile	aaa Lys	cac His	acg Thr	aac Asn 165	tgc Cys	agc Ser	aca Thr	594
ttt Phe	ggc Gly 170	ctc Leu	ctg Leu	cta Leu	att Ile	cag Gln 175	aaa Lys	gga Gly	aat Asn	gca Ala	aca Thr 180	cat His	gac Asp	aac Asn	tgt Cys	642
tgt Cys 185	tcc Ser	gga Gly	aac Asn	aga Arg	gaa Glu 190	gcc Ala	acg Thr	caa Gln	aag Lys	tgt Cys 195	gga Gly	ata Ile	gat Asp	gtc Val	acc Thr 200	690
ctg Leu	tgt Cys	gaa Glu	gag Glu	gcc Ala 205	ttc Phe	ttc Phe	agg Arg	ttt Phe	gct Ala 210	gtt Val	cct Pro	acc Thr	aag Lys	att Ile 215	ata Ile	738
cca Pro	aat Asn	tgg Trp	ctg Leu 220	agt Ser	gtt Val	ttg Leu	gtg Val	gac Asp 225	agt Ser	ttg Leu	cct Pro	ggg Gly	acc Thr 230	aaa Lys	gtg Val	786
aat Asn	gcc Ala	gag Glu 235	agt Ser	gta Val	gag Glu	agg Arg	ata Ile 240	aaa Lys	cgg Arg	aga Arg	cac His	agc Ser 245	tca Ser	caa Gln	gag Glu	834
caa Gln	acc Thr 250	ttc Phe	cag Gln	ctg Leu	ctg Leu	aag Lys 255	ctg Leu	tgg Trp	aaa Lys	cat His	caa Gln 260	aac Asn	aga Arg	gac Asp	cag Gln	882
gaa Glu 265	atg Met	gtg Val	aag Lys	aag Lys	atc Ile 270	atc Ile	caa Gln	gac Asp	att Ile	gac Asp 275	ctc Leu	tgt Cys	gaa Glu	agc Ser	agc Ser 280	930
gtg Val	cag Gln	cgg Arg	cat His	ctc Leu 285	ggc Gly	cac His	tcg Ser	aac Asn	ctc Leu 290	acc Thr	aca Thr	gag Glu	cag Gln	ctt Leu 295	ctt Leu	978
gcc Ala	ttg Leu	atg Met	gag Glu 300	agc Ser	ctg Leu	cct Pro	ggg Gly	aag Lys 305	aag Lys	atc Ile	agc Ser	cca Pro	gaa Glu 310	gag Glu	att Ile	1026
gag Glu	aga Arg	acg Thr 315	aga Arg	aag Lys	acc Thr	tgc Cys	aaa Lys 320	tcg Ser	agc Ser	gag Glu	cag Gln	ctc Leu 325	ctg Leu	aag Lys	cta Leu	1074
ctc Leu	agt Ser 330	tta Leu	tgg Trp	agg Arg	atc Ile	aaa Lys 335	aat Asn	ggt Gly	gac Asp	caa Gln	gac Asp 340	acc Thr	ttg Leu	aag Lys	ggc Gly	1122
ctg Leu 345	atg Met	tat Tyr	gcc Ala	ctc Leu	aag Lys 350	cac His	ttg Leu	aaa Lys	aca Thr	tcc Ser 355	cac His	ttt Phe	ccc Pro	aaa Lys	act Thr 360	1170
gtc Val	acc Thr	cac His	agt Ser	ctg Leu 365	agg Arg	aag Lys	acc Thr	atg Met	agg Arg 370	ttc Phe	ctg Leu	cac His	agc Ser	ttc Phe 375	aca Thr	1218
atg	tac	aga	ctg	tat	cag	aag	ctc	ttt	tta	gaa	atg	ata	ggg	aat	cag	1266

A-378CIP5C (3-31-04).ST25

Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln
 380 385 390

gtt caa tcc gtg aaa ata agc tgc tta taactaggaa tggtcactgg 1313
 Val Gln Ser Val Lys Ile Ser Cys Leu

gctgtttctt ca 1325

<210> 123
 <211> 401
 <212> PRT
 <213> Mus musculus

<400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile
 1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp
 20 25 30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
 50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys
 165 170 175

Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205

A-378CIP5C (3-31-04).ST25

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
 210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
 260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser
 275 280 285

Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly
 290 295 300

Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
 305 310 315 320

Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
 340 345 350

Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
 355 360 365

Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
 370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
 385 390 395 400

Leu

<210> 124
 <211> 1356
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (63)..(63)
 <223> At position 63, Y is a pyrimidine.

<220>
 <221> CDS
 <222> (95)..(1297)

A-378CIP5C (3-31-04).ST25

<400>	124															
gtatatataa	cgtgatgagc	gtacgggtgc	ggagacgcac	cggcgcgctc	gcccagccgc	60										
cgyc	tccaag	cccctgaggt	ttccggggac	caca	atg	aac	aag	ttg	ctg	tgc	tgc	115				
					Met	Asn	Lys	Leu	5							
gcg	ctc	gtg	ttt	ctg	gac	atc	tcc	att	aag	tgg	acc	acc	cag	gaa	acg	163
Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	
		10					15					20				
ttt	cct	cca	aag	tac	ctt	cat	tat	gac	gaa	gaa	acc	tct	cat	cag	ctg	211
Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	
	25					30					35					
ttg	tgt	gac	aaa	tgt	cct	cct	ggg	acc	tac	cta	aaa	caa	cac	tgt	aca	259
Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	
	40				45					50					55	
gca	aag	tgg	aag	tcc	gtg	tgc	gcc	cct	tgc	cct	gac	cac	tac	tac	aca	307
Ala	Lys	Trp	Lys	Ser	Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	
				60					65					70		
gac	agc	tgg	cac	acc	agt	gac	gag	tgt	cta	tac	tgc	agc	ccc	gtg	tgc	355
Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	
			75					80					85			
aag	gag	ctg	cag	tac	gtc	aag	cag	gag	tgc	aat	cgc	acc	cac	aac	cgc	403
Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	
		90					95					100				
gtg	tgc	gaa	tgc	aag	gaa	ggg	cgc	tac	ctt	gag	ata	gag	ttc	tgc	ttg	451
Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	
	105					110					115					
aaa	cat	agg	agc	tgc	cct	cct	gga	ttt	gga	gtg	gtg	caa	gct	gga	acc	499
Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	
	120				125					130					135	
cca	gag	cga	aat	aca	gtt	tgc	aaa	aga	tgt	cca	gat	ggg	ttc	ttc	tca	547
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	
				140					145					150		
aat	gag	acg	tca	tct	aaa	gca	ccc	tgt	aga	aaa	cac	aca	aat	tgc	agt	595
Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	
				155				160					165			
gtc	ttt	ggg	ctc	ctg	cta	act	cag	aaa	gga	aat	gca	aca	cac	gac	aac	643
Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	
		170					175					180				
ata	tgt	tcc	gga	aac	agt	gaa	tca	act	caa	aaa	tgt	gga	ata	gat	gtt	691
Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	
	185					190					195					
acc	ctg	tgt	gag	gag	gca	ttc	ttc	agg	ttt	gct	gtt	cct				

A-378CIP5C (3-31-04).ST25

Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Ala		
		250					255					260					
caa	gat	ata	gtc	aag	aag	atc	atc	caa	gat	att	gac	ctc	tgt	gaa	aac	931	
Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn		
	265					270					275						
agc	gtg	cag	cgg	cac	att	gga	cat	gct	aac	ctc	acc	ttc	gag	cag	ctt	979	
Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu		
	280				285					290					295		
cgt	agc	ttg	atg	gaa	agc	tta	ccg	gga	aag	aaa	gtg	gga	gca	gaa	gac	1027	
Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp		
				300					305					310			
att	gaa	aaa	aca	ata	aag	gca	tgc	aaa	ccc	agt	gac	cag	atc	ctg	aag	1075	
Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys		
			315					320					325				
ctg	ctc	agt	ttg	tgg	cga	ata	aaa	aat	ggc	gac	caa	gac	acc	ttg	aag	1123	
Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys		
		330					335					340					
ggc	cta	atg	cac	gca	cta	aag	cac	tca	aag	acg	tac	cac	ttt	ccc	aaa	1171	
Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys		
	345					350					355						
act	gtc	act	cag	agt	cta	aag	aag	acc	atc	agg	ttc	ctt	cac	agc	ttc	1219	
Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe		
	360				365					370					375		
aca	atg	tac	aaa	ttg	tat	cag	aag	tta	ttt	tta	gaa	atg	ata	ggt	aac	1267	
Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn		
				380					385					390			
cag	gtc	caa	tca	gta	aaa	ata	agc	tgc	tta	taactggaaa	tggccattga					1317	
Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu								
			395					400									
gctgttttcct	cacaattggc	gagatcccat	ggatgataa													1356	

<210> 125
 <211> 401
 <212> PRT
 <213> Homo sapiens

<400> 125

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
1 5 10 15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Ser Val Cys Ala Pro
50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

A-378CIP5C (3-31-04).ST25

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 85 90 95
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 100 105 110
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 115 120 125
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 165 170 175
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 180 185 190
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 210 215 220
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255
 Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln
 260 265 270
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 275 280 285
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 290 295 300
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
 305 310 315 320
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
 340 345 350

A-378CIP5C (3-31-04).ST25

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 126
<211> 139
<212> PRT
<213> Homo sapiens

<400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys
1 5 10 15

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
20 25 30

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala
35 40 45

Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys
50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr
65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn
85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His
100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly
115 120 125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys
130 135

<210> 127
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 127
acctacttct ttgaagagta gtcgacgaca cactatttac aggcggcc

48

<210> 128
<211> 219
<212> PRT
<213> Rattus rattus

<400> 128

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
210 215

<210> 129

A-378CIP5C (3-31-04).ST25

<211> 280
 <212> PRT
 <213> Rattus rattus

<400> 129

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Thr Arg Thr Gln Arg Trp Lys
 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
 245 250 255

A-378CIP5C (3-31-04).ST25

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr
275 280

<210> 130
<211> 207
<212> PRT
<213> Rattus rattus

<400> 130

Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly
1 5 10 15

Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp
20 25 30

Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr
35 40 45

Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys
50 55 60

Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val
65 70 75 80

Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys
85 90 95

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys
100 105 110

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys
115 120 125

Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr
130 135 140

Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro
145 150 155 160

Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn
165 170 175

Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Thr Ala Gly His Asn
180 185 190

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr
195 200 205

A-378CIP5C (3-31-04).ST25

<210> 131
 <211> 227
 <212> PRT
 <213> Rattus rattus

<400> 131

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Thr Thr Asp Gln
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190

Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr
 225

A-378CIP5C (3-31-04).ST25

<210> 132
 <211> 197
 <212> PRT
 <213> Rattus rattus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr
 1 5 10 15

Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu
 20 25 30

His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
 35 40 45

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
 50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
 85 90 95

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
 100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
 130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
 145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln
 165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met
 180 185 190

Arg Ala Leu Leu Val
 195

<210> 133
 <211> 208
 <212> PRT
 <213> Rattus rattus

<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
 1 5 10 15

A-378CIP5C (3-31-04).ST25

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

<210> 134
<211> 224
<212> PRT
<213> Rattus rattus

<400> 134

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
20 25 30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
35 40 45

A-378CIP5C (3-31-04).ST25

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
50 55 60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
65 70 75 80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
115 120 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

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<211> 202

<212> PRT

<213> Rattus rattus

<400> 135

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Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro
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Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val
35 40 45

Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro
50 55 60

A-378CIP5C (3-31-04).ST25

Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr
65 70 75 80

Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro
85 90 95

Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln
100 105 110

Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly
115 120 125

His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys
130 135 140

Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Val Cys
145 150 155 160

Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg Thr
165 170 175

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180 185 190

Ser Gln Leu Pro Ser Thr Pro Thr Leu Val
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<400> 136

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Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
Page 42

100

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
165 170 175

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180 185 190

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<213> Homo sapiens

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Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr
35 40 45

Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr
50 55 60

Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys
65 70 75 80

Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg
85 90 95

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100 105 110

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 35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro
 50 55 60

Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His
 65 70 75 80

Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe
 85 90 95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala
 100 105 110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe
 115 120 125

Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140

Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His
 145 150 155 160

Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile
 165 170 175

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
 180 185 190

Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly
 195 200 205

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser
 210 215 220

A-378CIP5C (3-31-04).ST25

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
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Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys
245 250 255

Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu
260 265 270

Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala
275 280 285

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile
290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Lys His Phe
325 330 335

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His
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Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
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A-378CIP5C (3-31-04).ST25

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Phe Pro Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly Arg Gln Leu
 20 25 30

Leu Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr
 35 40 45

A-378CIP5C (3-31-04).ST25

Val Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp Tyr Ser Tyr Thr
50 55 60

Asp Ser Trp His Thr Ser
65 70

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Tyr Leu His Tyr Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys
1 5 10 15

Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys
20 25 30

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35 40 45

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Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu
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Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala
20 25 30

Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp
35 40 45

Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys
50 55 60

Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val
Page 51

65

70

75

80

Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
85 90 95

His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro
100 105 110

Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn
115 120 125

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130 135

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35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro
50 55 60

Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His
65 70 75 80

Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe
85 90 95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala
100 105 110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe
115 120 125

Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn
130 135 140

Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His
145 150 155 160

Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile
165 170 175

A-378CIP5C (3-31-04).ST25

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
180 185 190

Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly
195 200 205

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser
210 215 220

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
225 230 235 240

Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys
245 250 255

Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu
260 265 270

Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro
275 280 285

Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu
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Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
305 310 315 320

Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe
325 330 335

Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His
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Page 53

A-378CIP5C (3-31-04).ST25

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A-378CIP5C (3-31-04).ST25

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A-378CIP5C (3-31-04).ST25

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gttacagatc cgtcgaggaa ctgaaaaacc agaaagttaa ctggtaagtt tagtcttttt	4620
gtcttttatt tcagggtccc gatccggtgg tggcgcgaaat caaagaactg ctctcagtg	4680
gatgttgccct ttacttctag gcctgtacgg aagtgttact tctgctctaa aagctgctgc	4740
aacaagcttc tagaccacc atg aac aag ttg ctg tgc tgc gcg ctc gtg ttt	4792
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe	
1 5 10	
ctg gac atc tcc att aag tgg acc acc cag gaa acg ttt cct cca aag	4840
Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys	
15 20 25	
tac ctt cat tat gac gaa gaa acc tct cat cag ctg ttg tgt gac aaa	4888
Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys	
30 35 40	
tgt cct cct ggt acc tac cta aaa caa cac tgt aca gca aag tgg aag	4936
Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys	
45 50 55	
acc gtg tgc gcc cct tgc cct gac cac tac tac aca gac agc tgg cac	4984
Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His	
60 65 70 75	
acc agt gac gag tgt cta tac tgc agc ccc gtg tgc aag gag ctg cag	5032
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln	
80 85 90	
tac gtc aag cag gag tgc aat cgc acc cac aac cgc gtg tgc gaa tgc	5080
Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys	
95 100 105	
aag gaa ggg cgc tac ctt gag ata gag ttc tgc ttg aaa cat agg agc	5128
Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser	
110 115 120	
tgc cct cct gga ttt gga gtg gtg caa gct gga acc cca gag cga aat	5176
Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn	
125 130 135	
aca gtt tgc aaa aga tgt cca gat ggg ttc ttc tca aat gag acg tca	5224
Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser	
140 145 150 155	
tct aaa gca ccc tgt aga aaa cac aca aat tgc agt gtc ttt ggt ctc	5272
Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu	
160 165 170	
ctg cta act cag aaa gga aat gca aca cac gac aac ata tgt tcc gga	5320
Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly	
175 180 185	
aac agt gaa tca act caa aaa gtc gac aaa act cac aca tgc cca ccg	5368

A-378CIP5C (3-31-04).ST25

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		190					195					200				
tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	5416
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	
	205					210					215					
cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	5464
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	
220					225					230					235	
tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	5512
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	
				240					245					250		
tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	5560
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	
			255					260					265			
gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	5608
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	
		270					275					280				
ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	5656
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	
	285					290					295					
aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	5704
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	
300					305					310					315	
ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	5752
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	
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gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	5800
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	
			335					340					345			
tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	5848
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	
		350					355					360				
aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	5896
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	
	365					370					375					
ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	5944
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	
380					385				390						395	
aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	5992
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	
				400					405					410		
acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggg	aaa	tgataactcg	ac				6037
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
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Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 Page 57

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Glu	Glu	Thr 35	Ser	His	Gln	Leu	Leu 40	Cys	Asp	Lys	Cys	Pro 45	Pro	Gly	Thr
Tyr	Leu 50	Lys	Gln	His	Cys	Thr 55	Ala	Lys	Trp	Lys	Thr 60	Val	Cys	Ala	Pro
Cys 65	Pro	Asp	His	Tyr	Tyr 70	Thr	Asp	Ser	Trp	His 75	Thr	Ser	Asp	Glu	Cys 80
Leu	Tyr	Cys	Ser	Pro 85	Val	Cys	Lys	Glu	Leu 90	Gln	Tyr	Val	Lys	Gln	Glu
Cys	Asn	Arg	Thr 100	His	Asn	Arg	Val	Cys 105	Glu	Cys	Lys	Glu	Gly 110	Arg	Tyr
Leu	Glu	Ile 115	Glu	Phe	Cys	Leu	Lys 120	His	Arg	Ser	Cys	Pro 125	Pro	Gly	Phe
Gly	Val 130	Val	Gln	Ala	Gly	Thr 135	Pro	Glu	Arg	Asn	Thr 140	Val	Cys	Lys	Arg
Cys 145	Pro	Asp	Gly	Phe	Phe 150	Ser	Asn	Glu	Thr	Ser 155	Ser	Lys	Ala	Pro	Cys 160
Arg	Lys	His	Thr	Asn 165	Cys	Ser	Val	Phe	Gly 170	Leu	Leu	Leu	Thr	Gln 175	Lys
Gly	Asn	Ala	Thr 180	His	Asp	Asn	Ile	Cys 185	Ser	Gly	Asn	Ser	Glu 190	Ser	Thr
Gln	Lys	Val 195	Asp	Lys	Thr	His	Thr 200	Cys	Pro	Pro	Cys	Pro 205	Ala	Pro	Glu
Leu	Leu 210	Gly	Gly	Pro	Ser	Val 215	Phe	Leu	Phe	Pro	Pro 220	Lys	Pro	Lys	Asp
Thr 225	Leu	Met	Ile	Ser	Arg 230	Thr	Pro	Glu	Val	Thr 235	Cys	Val	Val	Val	Asp 240
Val	Ser	His	Glu	Asp 245	Pro	Glu	Val	Lys	Phe 250	Asn	Trp	Tyr	Val	Asp 255	Gly
Val	Glu	Val	His 260	Asn	Ala	Lys	Thr	Lys 265	Pro	Arg	Glu	Glu	Gln 270	Tyr	Asn
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp

Page 58

275 A-378CIP5C (3-31-04).ST25
280 285

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
290 295 300

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
305 310 315 320

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
325 330 335

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
340 345 350

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
355 360 365

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
370 375 380

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
385 390 395 400

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
405 410 415

Ser Leu Ser Pro Gly Lys
420

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20 25 30

Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
35 40 45

Asp Trp His
50